

## EXHIBIT A

Primary screening to determine which core histone genes, when over-expressed, can enhance *Agrobacterium*-mediated transformation of *Arabidopsis*

Core Histone Gene	Total # of transformed plants screened	Individual line ID number with increased response to <i>Agrobacterium</i> -mediated transformation	
		Klett 0.1	Klett 0.01
HFO3	20	3; 4; 9; 11; 15; 19	3; 5; 15; 18; 19
HTA1	20	4; 6; 14; 16	6; 9; 14
HTA2	14	5; 11; 13	4; 5; 10; 11; 14
HTA3	18	2; 4; 5; 6; 7; 10; 11; 13; 14; 15; 19	1; 4; 5; 7; 9; 10; 11; 13; 14; 15; 17
HTA5	18	1; 5; 6; 11; 15; 16; 18	-
HTA6	5	5	1
HTA6	20	2; 4; 7; 9; 14; 17; 20	6; 9; 17; 20
HTA8	20	-	-
HTA10	-	-	-
HTB1	18	10; 12; 18	5; 8; 10; 15
HTB1	18	5; 8; 10; 15	8; 10; 12; 18
HTB3	6	-	-
HTB5	20	9	-
HTB8	20	6; 18; 20	1; 3; 7; 9
HTB9	9	9	5
HTB10	20	8	8
HTB11	20	13	15
HTR4	20	5; 10; 12	3; 4; 13; 17
HTR11	20	1; 2; 3; 4; 5; 7; 8; 10	7; 8; 16; 19; 20
HTR13	20	6; 11; 13; 16; 17	-

A total of 22 representative core histone genes were tested by expressing cDNAs of these genes under the CaMV 35S promoter in transgenic *Arabidopsis* plants. Infections were performed at a bacterial concentration of  $10^5$  cells/ml (Klett=0.01) or at  $10^6$  cells/ml (Klett=0.1).